STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/577,613_

Source: _TFWP,_

Date Processed by STIC: _05/11/2006_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual - ePAVE**)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>**ERROR DETECTED**</u>   <u>**SUGGESTED CORRECTION**</u>   **SERIAL NUMBER:** _____

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                        prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
   Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please
                        ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                        each n or Xaa can only represent a single residue.** Please present the maximum number of each
                        residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                        previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                        the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                        Artificial or Unknown sequences.**

7 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                        (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                        (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                        This sequence is intentionally skipped
                        Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
                        <400> sequence id number
                        000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                        In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                        is Artificial Sequence. (see item 11 below)

11 ____ Use of <220>   Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use
                        of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
                        Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
                        explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
                        Sequence Rules

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                        listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFWP

RAW SEQUENCE LISTING   DATE: 05/11/2006
PATENT APPLICATION: US/10/577,613   TIME: 11:18:49

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05112006\J577613.raw


```
   3 <110> APPLICANT: Alexander, Cherkasky
   5 <120> TITLE OF INVENTION: PCT/IB 2004/003536: CHERKASKY FUSION PROTEINS CONTAINING
ANTIBODY-,
   6       ANTIGEN - AND MICROTUBULE - BINDING REGIONS AND IMMUNE RESPONSE - TRIGGERIND
   7       REGIONS
   9 <130> FILE REFERENCE: -
:--> 11 <140> CURRENT APPLICATION NUMBER: US/10/577,613
:--> 11 <141> CURRENT FILING DATE: 2006-04-28
  11 <160> NUMBER OF SEQ ID NOS: 14
  13 <170> SOFTWARE: PatentIn version 3.3
  15 <210> SEQ ID NO: 1
  16 <211> LENGTH: 676
  17 <212> TYPE: PRT
:--> 18 <213> ORGANISM: Artifical sequence
4--> 20 <220> FEATURE:
4--> 20 <223> OTHER INFORMATION:
4--> 20 <400> 1
  22 Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu
  23 1               5                   10                  15
  26 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser
  27             20                  25                  30
  30 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys
  31         35                  40                  45
  34 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys
  35     50                  55                  60
  38 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
  39 65                  70                  75                  80
  42 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
  43                 85                  90                  95
  46 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
  47             100                 105                 110
  50 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
  51         115                 120                 125
  54 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
  55     130                 135                 140
  58 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
  59 145                 150                 155                 160
  62 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
  63                 165                 170                 175
  66 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
  67             180                 185                 190
  70 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
  71         195                 200                 205
  74 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
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RAW SEQUENCE LISTING   DATE: 05/11/2006
PATENT APPLICATION: US/10/577,613   TIME: 11:18:49

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05112006\J577613.raw

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75      210                 215                 220
78 Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
79 225                 230                 235                 240
82 Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly Gly Gly Gly
83                 245                 250                 255
86 Gly Met Ser Pro Phe Pro Leu Thr Ser Met Asp Lys Ala Phe Ile Thr
87                 260                 265                 270
90 Val Leu Glu Met Thr Pro Val Leu Gly Thr Glu Ile Ile Asn Tyr Arg
91             275                 280                 285
94 Asp Gly Met Gly Arg Val Leu Ala Gln Asp Val Tyr Ala Lys Asp Asn
95         290                 295                 300
98 Leu Pro Pro Phe Pro Ala Ser Val Lys Asp Gly Tyr Ala Val Arg Ala
99 305                 310                 315                 320
102 Ala Asp Gly Pro Gly Asp Arg Phe Ile Ile Gly Glu Ser Gln Ala Gly
103                 325                 330                 335
106 Glu Gln Pro Thr Gln Thr Val Met Pro Gly Gln Val Met Arg Val Thr
107             340                 345                 350
110 Thr Gly Ala Pro Ile Pro Cys Gly Ala Asp Ala Val Val Gln Val Glu
111         355                 360                 365
114 Asp Thr Glu Leu Ile Arg Glu Ser Asp Asp Gly Thr Glu Glu Leu Glu
115 370                 375                 380
118 Val Arg Ile Leu Val Gln Ala Arg Pro Gly Gln Asp Ile Arg Pro Ile
119 385                 390                 395                 400
122 Gly His Asp Ile Lys Arg Gly Glu Cys Val Leu Ala Lys Gly Thr His
123             405                 410                 415
126 Met Gly Pro Ser Glu Ile Gly Leu Leu Ala Thr Val Gly Val Thr Glu
127         420                 425                 430
130 Val Glu Val Asn Lys Phe Pro Val Val Ala Val Met Ser Thr Gly Asn
131         435                 440                 445
134 Glu Leu Leu Asn Pro Glu Asp Asp Leu Leu Pro Gly Lys Ile Arg Asp
135 450                 455                 460
138 Ser Asn Arg Ser Thr Leu Leu Ala Thr Ile Gln Glu His Gly Tyr Pro
139 465                 470                 475                 480
142 Thr Ile Asn Leu Gly Ile Val Gly Asp Asn Pro Asp Asp Leu Leu Asn
143             485                 490                 495
146 Ala Leu Asn Glu Gly Ile Ser Arg Ala Asp Val Ile Ile Thr Ser Gly
147         500                 505                 510
150 Gly Val Ser Met Gly Glu Lys Asp Tyr Leu Lys Gln Val Leu Asp Ile
151         515                 520                 525
154 Asp Leu His Ala Gln Ile His Phe Gly Arg Val Phe Met Lys Pro Gly
155     530                 535                 540
158 Leu Pro Thr Thr Phe Ala Thr Leu Asp Ile Asp Gly Val Arg Lys Ile
159 545                 550                 555                 560
162 Ile Phe Ala Leu Pro Gly Asn Pro Val Ser Ala Val Val Thr Cys Asn
163             565                 570                 575
166 Leu Phe Val Val Pro Ala Leu Arg Lys Met Gln Gly Ile Leu Asp Pro
167         580                 585                 590
170 Arg Pro Thr Ile Ile Lys Ala Arg Leu Ser Cys Asp Val Lys Leu Asp
171     595                 600                 605
```

```
174 Pro Arg Pro Glu Tyr His Arg Cys Ile Leu Thr Trp His His Gln Glu
175     610                 615                 620
178 Pro Leu Pro Trp Ala Gln Ser Thr Gly Asn Gln Met Ser Ser Arg Leu
179 625                 630                 635                 640
182 Met Ser Met Arg Ser Ala Asn Gly Leu Leu Met Leu Pro Pro Lys Thr
183                 645                 650                 655
186 Glu Gln Tyr Val Glu Leu His Lys Gly Glu Val Val Asp Val Met Val
187                 660                 665                 670
190 Ile Gly Arg Leu
191         675
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 2092
196 <212> TYPE: DNA
197 <213> ORGANISM: Artifical sequence        Same error
199 <220> FEATURE:
199 <223> OTHER INFORMATION:
199 <400> 2
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202 cttaaatgct gatcaacgca atggttttat ccaaagcctt aaagatgatc caagccaaag     120
204 tgctaacgtt ttaggtgaag ctaaaaaatt aaacgaatct caagcaccga aagctgacaa     180
206 caatttcaac aaagaacaac aaaatgcttt ctatgaaatc ttgaacatgc ctaacttgaa     240
208 cgaagaacaa cgcaatggtt tcatccaaag cttaaaagat gacccaagtc aaagtgctaa     300
210 cctattgtca gaagctaaaa agttaaatga atctcaagca ccgaaagcgg ataacaaatt     360
212 caacaaagaa caacaaaatg ctttctatga aatcttacat ttacctaact aaacgaaga      420
214 acaacgcaat ggtttcatcc aaagcctaaa agatgaccca agccaaagcg ctaacctttt     480
216 agcagaagct aaaaagctaa atgatgcaca agcaccaaaa gctgacaaca aattcaacaa     540
218 agaacaacaa aatgctttct atgaaatttt acatttacct aacttaactg aagagcaacg     600
220 taacggcttc atccaaagcc ttaaagacga tccttcagtg agcaaagaaa ttttagcaga     660
222 agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa gacaacaaca aacctggtaa     720
224 agaagacggc aacaaacctg gcaaagaaga cggtaacggc ggcggcggcg gcgtttaggt     780
226 cacagtgctg tcgatatcac caaggtggct agaagacatc gcatgtctcc ttttcctctg     840
228 acatctatgg acaaagcctt tatcacagtc ctggagatga ctccggtgct tgggacagaa     900
230 atcatcaatt accgagatgg aatggggcga gtccttgctc aagatgtata tgcaaaagac     960
232 aatttacccc ccttcccagc atcagtaaaa gatggctatg ctgtccgagc tgctgatggc    1020
234 ccaggagatc gtttcatcat tggggaatcc caagctggtg aacagccaac tcagacagta    1080
236 atgccaggac aagtcatgcg ggttacaaca ggtgctccaa taccctgcgg tgctgatgca    1140
238 gtagtacaag tggaagatac cgaacttatc agggaatcag atgatggcac tgaagaactt    1200
240 gaagtgcgaa ttctggtgca agctcggcca ggccaagata tcagacccat cggccatgac    1260
242 attaaagag gggaatgtgt tttggccaaa ggaacccaca tgggcccctc agagattggt    1320
244 cttctggcaa ctgtaggtgt cacagaggtt gaagttaata agtttccagt ggttgcagtc    1380
246 atgtcaacag gaatgagct gctaaatcct gaagatgacc tcttaccagg gaagattcga    1440
248 gacagcaatc gttcaactct tctagcaaca attcaggaac atggttaccc cacgatcaac    1500
250 ttgggtattg taggagacaa cccagatgac ttactcaatg ccttgaatga gggtatcagt    1560
252 cgtgctgatg tcatcatcac atcaggggt gtatccatgg gggaaaagga ctatctcaag    1620
254 caggtgctgg acattgatct tcatgctcag atccattttg gcagggtttt tatgaaacca    1680
256 ggcttgccaa caacatttgc aactttggat attgatggtg taagaaaaat aatctttgca    1740
258 ctacctggga tcctgtatc ggctgtggtc acctgcaatc tctttgttgt gcctgcactg    1800
260 aggaaaatgc agggcatctt ggatcctcgg ccaaccatca tcaaagcaag gttatcatgt    1860
262 gatgtaaaac ttgatcctcg tccagaatac catcggtgta tactaacttg gcatcaccaa    1920
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264 gaaccactac cttgggcaca gagtacaggt aatcaaatga gcagccgtct gatgagcatg    1980
266 cgcagtgcca atggattgtt gatgctacct ccaaagacag aacagtacgt ggagctccac    2040
268 aaaggcgagg tggtggatgt catggtcatt ggacggctat gatggtcacc ag            2092
271 <210> SEQ ID NO: 3
272 <211> LENGTH: 300
273 <212> TYPE: PRT
274 <213> ORGANISM: Artifical sequence
277 <220> FEATURE:
278 <221> NAME/KEY: misc_feature
279 <222> LOCATION: (264)..(264)
280 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
282 <220> FEATURE:
283 <221> NAME/KEY: misc_feature
284 <222> LOCATION: (278)..(278)
285 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
287 <220> FEATURE:
288 <221> NAME/KEY: misc_feature
289 <222> LOCATION: (281)..(281)
290 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
292 <400> SEQUENCE: 3
294 Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu
295 1               5                   10                  15
298 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser
299             20                  25                  30
302 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys
303         35                  40                  45
306 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys
307     50                  55                  60
310 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
311 65                  70                  75                  80
314 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
315                 85                  90                  95
318 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
319             100                 105                 110
322 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
323         115                 120                 125
326 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
327     130                 135                 140
330 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
331 145                 150                 155                 160
334 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
335             165                 170                 175
338 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
339             180                 185                 190
342 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
343         195                 200                 205
346 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
347     210                 215                 220
350 Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
```

RAW SEQUENCE LISTING   DATE: 05/11/2006
PATENT APPLICATION: US/10/577,613   TIME: 11:18:49

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05112006\J577613.raw

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    351 225                   230                   235                   240
    354 Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly Gly Gly Gly
    355                   245                   250                   255
W--> 358 Gly Ala Ala Ala Ser Thr Ala Xaa Ala Ser Thr Ala Lys Glu Thr Ala
    359                   260                   265                   270
W--> 362 Glu Ala Val Ala Asp Xaa Ile Leu Xaa Lys Ala Gly Pro Leu Val Ala
    363           275                   280                   285
    366 Val Ser Ala Val Ala Leu Asp Ile Thr Ala Tyr Pro
    367       290                   295                   300
    370 <210> SEQ ID NO: 4
    371 <211> LENGTH: 912
    372 <212> TYPE: DNA
C--> 373 <213> ORGANISM: Artifical sequence
    376 <220> FEATURE:
    377 <221> NAME/KEY: misc_feature
    378 <222> LOCATION: (792)..(792)
    379 <223> OTHER INFORMATION: n is a, c, g, t or u
    381 <220> FEATURE:
    382 <221> NAME/KEY: misc_feature
    383 <222> LOCATION: (835)..(835)
    384 <223> OTHER INFORMATION: n is a, c, g, t or u
    386 <220> FEATURE:
    387 <221> NAME/KEY: misc_feature
    388 <222> LOCATION: (844)..(844)
    389 <223> OTHER INFORMATION: n is a, c, g, t or u
    391 <400> SEQUENCE: 4
    392 tgctgcgcaa cacgatgaag ctcaacaaaa cgctttttat caagtcttaa atatgcctaa   60
    394 cttaaatgct gatcaacgca atggttttat ccaaagcctt aaagatgatc caagccaaag  120
    396 tgctaacgtt ttaggtgaag ctaaaaaatt aaacgaatct caagcaccga aagctgacaa  180
    398 caatttcaac aaagaacaac aaaatgcttt ctatgaaatc ttgaacatgc ctaacttgaa  240
    400 cgaagaacaa cgcaatggtt tcatccaaag cttaaaagat gacccaagtc aaagtgctaa  300
    402 cctattgtca gaagctaaaa agttaaatga atctcaagca ccgaaagcgg ataacaaatt  360
    404 caacaaagaa caacaaaatg ctttctatga aatcttacat ttacctaact taaacgaaga  420
    406 acaacgcaat ggtttcatcc aaagcctaaa agatgaccca agccaaagcg ctaacctttt  480
    408 agcagaagct aaaaagctaa atgatgcaca agcaccaaaa gctgacaaca aattcaacaa  540
    410 agaacaacaa aatgctttct atgaaatttt acatttacct aacttaactg aagagcaacg  600
    412 taacggcttc atccaaagcc ttaaagacga tccttcagtg agcaaagaaa ttttagcaga  660
    414 agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa gacaacaaca acctggtaa   720
    416 agaagacggc aacaaacctg gcaaagaaga cggtaacggc ggcggcggcg gcgcggccgc  780
W--> 418 gtcgaccgcg gncgcgtcga cggcaaagga gactgctgag gctgttgctg atganatact  840
W--> 420 gganaaggct gggccacttg ttgctgtgtc tgctgttgca cttgatataa ctgcctaccc  900
    422 ctaaaagcca aa                                                       912
    425 <210> SEQ ID NO: 5
    426 <211> LENGTH: 3718
    427 <212> TYPE: DNA
C--> 428 <213> ORGANISM: Artifical sequence
W--> 430 <220> FEATURE:
W--> 430 <223> OTHER INFORMATION:
W--> 430 <400> 5
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[handwritten annotation:] → Same Error

[handwritten annotation:] → Same Error

[handwritten annotation in oval:] The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/11/2006
PATENT APPLICATION: **US/10/577,613**   TIME: 11:18:50

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\05112006\J577613.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 264,278,291
Seq#:4; N Pos. 792,835,844
Seq#:8; N Pos. 488,531,540
Seq#:9; N Pos. 440,483,492
Seq#:12; N Pos. 792,835,844

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:1,2,5,6,7,10,11,13,14

VERIFICATION SUMMARY   DATE: 05/11/2006
PATENT APPLICATION: US/10/577,613   TIME: 11:18:50

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05112006\J577613.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:18 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:20 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:20 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:20 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:20
L:197 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:199 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:199
L:274 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:256
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:272
L:373 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:780
L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:840
L:428 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:430 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:430 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:430 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:430
L:559 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:561 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:561 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:561 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:561
L:652 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:654 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:654 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:654 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:654
L:743 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:480
L:812 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420
L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:480
L:881 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:883 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:883 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:883 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:883
L:1028 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:1030 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:1030 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>

ORGANISM:Artificial Sequence
L:1030 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1030
L:1173 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:1218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:780
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:840
L:1252 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:1254 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:1254 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:1254 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:1254

VERIFICATION SUMMARY   DATE: 05/11/2006
PATENT APPLICATION: US/10/577,613   TIME: 11:18:50

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\05112006\J577613.raw**

L:1355 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:1357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:1357 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:1357 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:1357